

Result No.	Score	Query	Match	Length	DB	ID	Description
1	4880	99.3	919	1	ANDR_HUMAN	P10775	homo sapien
2	4794	97.6	911	1	ANDR_PANTHERA	097775	pan troglodytes
3	4694	95.6	895	1	ANDR_PAPHA	097502	papiro hamadryas
4	4678	95.2	895	1	ANDR_MACACA	097766	macaca fasciata
5	4445	89.7	884	1	ANDR_EULEMUR	097776	eulemur fulvus
6	4319	87.9	907	1	ANDR_CANFALIS	P15207	canis familiaris
7	4200	85.5	902	1	ANDR_RAT	P19091	rattus norvegicus
8	4176	85.0	899	1	ANDR_MOUSE	P49599	mus musculus
9	3109	71.4	709	1	PRGR_RABBIT	P06186	oryctolagus cuniculus
10	1262	25.7	930	1	PRGR_HUMAN	P05601	homo sapiens
11	1234	25.1	923	1	PRGR_PIG	Q63449	rattus norvegicus
12	1218	24.8	786	1	PRGR_CHICK	P07812	gallus gallus
13	1116	22.7	923	1	PRGR_MOUSE	Q00175	mus musculus
14	1092	22.2	981	1	PRGR_SHEEP	Q25950	ovis aries
15	1078	22.0	984	1	MCR_RAT	P22199	rattus norvegicus
16	1069	21.8	795	1	MCR_HUMAN	P08235	homo sapiens
17	1063	21.5	21.7			P05536	rattus norvegicus
18	1053	21.4	783	1	GCR_MOUSE	Q91573	mus musculus
19	1053	21.4	776	1	GCR_XENLIA	P49844	xenopus laevis
20	1053	21.4	777	1	GCR_SAGOE	P79269	saguinus oedipus
21	1046	21.3	777	1	GCR_AOTNA	P79686	aotus nancymai
22	1042	21.2	777	1	GCR_SAITH	P04150	homo sapiens
23	1042	21.2	778	1	GCR_SAITH	Q46567	saimiri sciureus
24	1041	21.2	777	1	GCR_SAITH	Q13186	saimiri boliviensis
25	1041	21.2	777	1	GCR_SAITH	Q95267	tupaiasalatana
26	1033	21.1	612	1	MCR_XENLIA	P49843	oncorhynchus tshawytscha
27	1033	21.0	776	1	GCR_TUPGB	Q29131	tupaiasalatana
28	1023	20.8	758	1	CR_ONCMB	P49115	cavia porcellus
29	1014	20.6	977	1	MCR_TUPGB	P73673	oncorhynchus tshawytscha
30	1005	20.5	807	1	GCR_PAOLI	P49115	cavia porcellus
31	996	20.3	771	1	GCR_CAVPO	P73673	oncorhynchus tshawytscha
32	970	19.8	703	1	GCR_PIG	P73733	macropus eu
33	509	10.4	180	1	PRGR_MACBEU	P73733	macropus eu

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
ANDR_HUMAN
ID ANDR_HUMAN
STANDARD;
PRT; 919 AA.
AC P10775;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR).
GN AR OR NP3C4 OR DMR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE:89112208; PubMed=3216866;
RA Lubahn D.B., Joseph D.R., Sar M., Tan J., Higgs H.N., Larson R.E.,
RA French F.S., Wilson E.M.;
RT "The human androgen receptor: complementary deoxyribonucleic acid
cloning, sequence analysis and gene expression in prostate.",
RL Mol. Endocrinol. 2:1265-1275 (1988).
RN [2]
RN SEQUENCE FROM N.A. AND VARIANT CA1S MET-866.
RX MEDLINE:90083302; PubMed=239473;
RA Lubahn D.B., Brown T.R., Simental J.A., Higgs H.N., Migeon C.J.,
RA Wilson E.M., French F.S.;
RT "Sequence of the intron/exon junctions of the coding region of the
human androgen receptor gene and identification of a point mutation
in a family with complete androgen insensitivity.",
RN Proc. Natl. Acad. Sci. U.S.A. 86:9534-9538 (1989).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=90258935; PubMed=2342476;
RA Govindan M.V.;
RT "Specific region in hormone-binding domain is essential for hormone
binding and trans-activation by human androgen receptor.",
RL Mol. Endocrinol. 4:417-422 (1990).
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=8917168; PubMed=1174628;
RA Chang C., Kokontis J., Liao S.;
RT "Structural analysis of complementary DNA and amino acid sequences of
human and rat androgen receptors.",
RL Proc. Natl. Acad. Sci. U.S.A. 85:7211-7215 (1988).
RN [5]
RN SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=89098909; PubMed=2911578;
RA Tille W.D., Marcelli M., Wilson J.D., McPhaul M.J.;
RT "Characterization and expression of a cDNA encoding the human androgen
receptor.",
RL Proc. Natl. Acad. Sci. U.S.A. 86:327-331 (1989).
RN [6]
RN SEQUENCE FROM N.A.
RC TISSUE=Prostate;

RP REVIEW ON VARIANTS. MEDLINE=91155943; PubMed=2293020; PMID=2293020; PubMed=7937057; RX MEDLINE=9523089; PubMed=7626493; RX MEDLINE=9532489; PubMed=7626493; RA Patterson M.N., Hughes L.A., Gottlieb B., Pinsky L.; RA "The androgen receptor gene database." RT "Definition of the human androgen receptor gene structure permits the identification of mutations that cause androgen resistance: premature termination of the receptor protein at amino acid residue 588 causes complete androgen resistance." RT Moll. Endocrinol. 4:1105-1116 (1990). X
RN [7] X
SEQUENCE OF 189-919 FROM N.A. RT
MEDLINE=88178111; PubMed=3353726; RA
Chang C., Kokontis J., Liao S.; RA
"Molecular cloning of human and rat complementary DNA encoding androgen receptors." RT
Science 240:324-326 (1988). ?
RN [8] X
SEQUENCE OF 468-919 FROM N.A. RT
MEDLINE=88240407; PubMed=3377788; RX
Trapman J., Klaassen P., Kuiper G.G.J.M., van der Korput J.A.G.M., RA
Faber P.W., van Rooij H.C.J., Geurts van Kessel A., Voorhorst M.M., RA
Mulder E., Brinkmann A.O., RA
"Cloning, structure and expression of a cDNA encoding the human androgen receptor." RT
Biochem. Biophys. Res. Commun. 153:241-246 (1988). ?
RN [9] X
POLYMORPHISM OF POLY-GLN REGION. RT
MEDLINE=92220629; PubMed=1561105; RX
Sleddens H.F.B.M., Oostra B.A., Brinkmann A.O., Trapman J.; RA
"Trinucleotide repeat polymorphism in the androgen receptor gene (AR)." RT
Nucleic Acids Res. 20:1427-1427 (1992). X
RN [10] X
POLYMORPHISM OF POLY-GLY REGION. RT
Submitted (Feb-1995) to the EMBL/GenBank/DBDJ databases. X
RN [11] X
POLYMORPHISM OF POLY-GLN REGION. RT
MEDLINE=97250535; PubMed=9096391; RX
Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Brufsky A., RA
Talcott J., Henneken C.H., Kantoff P.W.; RA
"The CAG repeat within the androgen receptor gene and its relation to prostate cancer." RT
Proc. Natl. Acad. Sci. U.S.A. 94:3320-3323 (1997). X
RN [12] X
ERRATUM. RT
Giovannucci E., Stampfer M.J., Krithivas K., Brown M., Dahl D., RA
Brufsky A., Talcott J., Henneken C.H., Kantoff P.W., Wilson J.D., RA
Proc. Natl. Acad. Sci. U.S.A. 94:8272-8272 (1997). X
RN [13] X
REVIEW ON VARIANTS. RT
MEDLINE=93109259; PubMed=1458719; RX
Pinsky L., Trifiro M.A., Kaufman M., Beitel L.K., Mhatre A., RA
Kazemi-Esfarjani P., Sabaghian N., Lumbroso R., Alvarezado C., RA
Vasilic M., Gottlieb B.; RA
"Androgen resistance due to mutation of the androgen receptor." RT
Clin. Invest. Med. 15:456-472 (1992). X
RN [14] X
REVIEW ON VARIANTS. RT
MEDLINE=93339360; PubMed=83339746; RX
Brown T.R., Scherer P.A., Chang Y.-T., Migeon C.J., Ghirri P., RA
Murroni K., Zhou Z.; RA
"Molecular genetics of human androgen insensitivity." RT
Eur. J. Pediatr. 152 Suppl. 2:S62-S69 (1993). X
RN [15] X
REVIEW ON VARIANTS. RT
MEDLINE=94059770; PubMed=8240973; RX
Sultani C., Lumbroso S., Poujol N., Belon C., Boudon C., RA
"Mutations of androgen receptor gene in androgen insensitivity syndromes." RT
J. Steroid Biochem. Mol. Biol. 46:519-520 (1993). X
RN [16] X
RP REVIEW ON VARIANTS. RX
MEDLINE=91169385; PubMed=9016528; RX
Gottlieb B., Trifiro M.A., Lumbroso R., Vasilic M., Pinsky L.; RA
"Androgen receptor gene mutations." RT
J. Steroid Biochem. Mol. Biol. 53:443-448 (1995). X
RN [17] X
REVIEW ON VARIANTS. RX
MEDLINE=91169385; PubMed=9016528; RX
Brinkmann A.O., Jenster G., Ris-Stalpers C., van der Korput J.A.G.M., RA
Bruylants H.T., Boehmer A.L.M., Trapman J.; RA
"Androgen receptor mutations." RT
J. Steroid Biochem. Mol. Biol. 53:3560-3567 (1994). X
RN [18] X
REVIEW ON VARIANTS. RX
MEDLINE=91169385; PubMed=9016528; RX
Gottlieb B., Trifiro M.A., Lumbroso R., Vasilic M., Pinsky L.; RA
"The androgen receptor gene database." RT
Nucleic Acids Res. 25:158-158 (1997). X
RN [19] X
VARIANT LNCAP ALA-877. RX
MEDLINE=91083633; PubMed=2260966; RX
Veldscholte J., Ris-Stalpers C., Kuiper G.G.J.M., Jenster G., RA
Berrevoets C.A., Claassen E., van Rooij H.C.J., Trapman J., RA
Brinkmann A.O., Mulder E.; RA
"A mutation in the ligand binding domain of the androgen receptor of human LNCAP cells affects steroid binding characteristics and response to anti-androgens." RT
Biochem. Biophys. Res. Commun. 173:534-540 (1990). X
RN [20] X
VARIANT CAIS CYS-774; GLN-831 AND MET-866. RX
Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J., RA
Corfen J.L.; RA
"Functional characterization of naturally occurring mutant androgen receptors from subjects with complete androgen insensitivity." RT
Mol. Endocrinol. 4:1759-1772 (1990). X
RN [21] X
VARIANT CYS-774. RX
MEDLINE=91186983; PubMed=2082719; RX
Brown T.R., Lubahn D.B., Wilson E.M., French F.S., Migeon C.J., RA
Corfen J.L.; RA
"Functional characterization of naturally occurring mutant androgen receptors from subjects with complete androgen insensitivity." RT
Mol. Endocrinol. 4:1759-1772 (1990). X
RN [22] X
VARIANT CAIS PRO-617. RX
MEDLINE=91154385; PubMed=1999491; RX
Marcelli M., Zoppi S., Grino P.B., Griffin J.E., Wilson J.D., RA
"A mutation in the DNA-binding domain of the androgen receptor gene causes complete testicular feminization in a patient with receptor-positive androgen resistance." RT
J. Clin. Invest. 87:1123-1126 (1991). X
RN [23] X
VARIANT CAIS CYS-763. RX
MEDLINE=91185626; PubMed=2010552; RX
Marcelli M.J., Marcelli M., Tilley W.D., Griffin J.E., Wilson J.D., RA
"A mutation in the DNA-binding domain of the androgen receptor gene causes complete testicular feminization in a patient with receptor-positive androgen resistance." RT
J. Clin. Invest. 87:1413-1414 (1991). X
RN [24] X
VARIANT CAIS ASN-695 AND HIS-695, AND SEQUENCE OF 629-723 FROM N.A. RX
MEDLINE=22131007; PubMed=1775137; RX
Ris-Stalpers C., Trifiro M.A., Kuiper G.G.J.M., Jenster G., Romalo G., RA
Sai T., van Rooij H.C.J., Kaufman M., Rosenfeld R.L., Liao S., RA
Schweikert H.-U., Trapman J., Pinsky L., Brinkmann A.O., RA
"Substitution of aspartic acid 686 by histidine or asparagine in the human androgen receptor leads to a functionally inactive protein with altered hormone-binding characteristics." RT
J. Steroid Biochem. Mol. Biol. 46:519-520 (1993). X
RN [25] X

CC	- - DOMAIN: SUBCELLULAR LOCATION: NUCLEAR.
CC	- - DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC	- - SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC	- - NR3 SUBFAMILY.
CC	-----
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CC	-----
DR	U94179; AAC73050.1; -
DR	HSSP; P06536; 1RGD.
DR	InterPro; IPR0110103; Androgen_recep.
DR	InterPro; IPR000536; Hormone_rec_19.
DR	InterPro; IPR001628; zf-C4.
DR	Pfam; PF02166; Androgen_recep; 1.
DR	Pfam; PF00104; hormone_rec; 1.
DR	Pfam; PF04105; zf-C4; 1.
DR	PRINTS; PRO0047; STROUDINGER.
DR	PRINTS; PRO0521; ANDROGENR.
DR	SMART; SM00430; HOLI; 1.
DR	SMART; SM00399; Znf_C4; 1.
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW	Receptor; translocation regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
FT	DOMAIN 1 533 MODULATING (BY SIMILARITY).
FT	DNA_BIND 535 600 NUCLEAR RECEPTOR-TYPE.
FT	ZN_FING 535 555 C4-TYPE.
FT	ZN_FING 571 595 C4-TYPE.
FT	DOMAIN 666 895 LIGAND-BINDING.
FT	DOMAIN 55 62 POLY-GUN.
FT	DOMAIN 68 74 POLY-GUN.
FT	DOMAIN 178 182 POLY-GUN.
FT	DOMAIN 357 366 POLY -PRO.
FT	DOMAIN 381 387 POLY -ALA.
FT	DOMAIN 434 448 POLY -GLY.
SQ	SEQUENCE 895 AA; 96494 MW; A3E17916F43A907 CRC64;
Query	Match 95.2%; Score 4678; DB 1; Length 895;
Best	Local Similarity 95.9%; Pred. No. 2.6e-214;
Matches	886; Conservative 2; Mismatches 6; Indels 30; Gaps 3;
Db	1 MEVOLGLGRVYPRPSKTYGAFQNLQFQSREVITQNPGRPHPEASAPPAGASLLLQQQ 60
Db	1 MEVOLGLGRVYPRPSKTYGAFQNLQFQSREVITQNPGRPHPEASAPPAGASLLLQQQ 54
Qy	61 QQQQQQQQQQQQQQQQQQQQQQQQSPR -QQQQQQEDGSPQAHRGPtgYLVLDEEQQPS 119
Db	55 ----- QQQQQQQQQSPRQQQQQEDGSPQAHRGPtgYLVLDEEQQPS 119
Qy	120 QPQSALECHPERGVCEPGAAVAAASKGLPQLQAPPDDDSAPSPSTLSSGGRAREASGPTSSKDNYLGGTSTISDNAK 179
Db	101 QPQSAECPHCEPERGVCEPGAAVAAAGKGLPQLQAPPDDDSAPSPSTLSSGGRAREASGPTSSKDNYLGGTSTISDNAK 160
Qy	180 SADLDLSSASTMQLQQQQAEVSEGSSEGRAREASGPTSSKDNYLGGTPTFPGLSSC 239
Db	161 STDLKDLSASTMQLQQQQAEVSEGSSEGRAREASGPTSSKDNYLGGTSTISDNAK 220
Qy	240 ELCRAVSVNGLGVBALEHLSPEQLRGDCMYAQLPGYPPAVRTPCPAIAECKGSLDD 299
Db	221 ELCRAVSVNGLGVBALEHLSPEQLRGDCMYAQLPGYPPAVRTPCPAIAECKGSLDD 280
Qy	300 SAGKSTEDTAEYSPFKGGTYTKGLEGESLGCSAAGSSGTELPSLTSLSIKSGALDEA 359
Db	281 SAGKSTEDTAEYSPFKGGTYTKGLEGESLGCSAAGSSGTELPSLTSLSIKSGALDEA 340
Qy	360 AYQRSDYYNFPPLAGPPPPPPPHARIKLKENPLDYLGSWAAAAAQCRLYDLSLHGA 419

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Qy	540 DMRLETARDHVLPIDYFPPQKTCILCIGDEASGCHYGAFTGCKVFFKRAEGKOKYLC 599 : : : : : : : : : : : : Db	501 DMRLETARDHVLPIDYFPPQKTCILCIGDEASGCHYGAFTGCKVFFKRAEGKOKYLC 560 DR SMART; SMART; ZnF_C4; 1.
Qy	600 ASRNDCTIDKFRKNCPSCLRKCYEAGMTLCAKRLKKLGNLKLQBEGEASSTTSPEET 659 : : : : : : : : : : : Db	561 ASRNDCTIDKFRKNCPSCLRKCYEAGMTLCAKRLKKLGNLKLQBEGEASATSTPEES 620 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1. KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
Qy	660 TQKLTVSHIEGECOPFLNVLEAIEFGVVCAGHDNNQPDSTAAALLSLNLGERQLVHV 719 : : : : : : : : : Db	621 SQKLTVSHIEGECOPFLNVLEAIEFGVVCAGHDNNQPDSTAAALLSLNLGERQLVHV 680 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1. KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
Qy	720 VPKAKALPGFRNLHVDDQMAV1QYSWNLVYAMGWRSTFNSRMLYFADLVENEYRM 779 : : : Db	681 VPKAKALPGFRNLHVDDQMAV1QYSWNLVYAMGWRSTFNSRMLYFADLVENEYRM 740 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1. KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
Qy	780 HKSRMYSOCVVRMRHLSOEGFWLQITPOEFLCMKALLLFSIIPVPGLKKNQKFDELRMNYI 839 : : : Db	741 HKSRMYSOCVVRMRHLSOEGFWLQITPOEFLCMKALLLFSIIPVPGLKKNQKFDELRMNYI 800 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1. KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
Qy	840 KELDRITACKRNPNTCSRSRYYQLTLDLSSVPIARELQFTFDLKLHKMSVYDFPEMM 899 : : : Db	801 KELDRITACKRNPNTCSRSRYYQLTLDLSSVPIARELQFTFDLKLHKMSVYDFPEMM 860 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1. KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
Qy	900 AETISVQVPKTKLSGKVPKIYHTQ 923 : : Db	861 AETISVQVPKTKLSGKVPKIYHTQ 884 DR PROSITE; PS0031; NUCLEAR RECEPTOR; 1. KW Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
RESULT 6		
	ANDR_CANFA	STANDARD; PRT; 907 AA.
AC	ACID ANDR_CANFA	
DT	30-MAY-2000 (Rel. 39, Created)	
DT	30-MAY-2000 (Rel. 39, Last sequence update)	
DT	30-MAY-2000 (Rel. 39, Last annotation update)	
DE	ANDROGIN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR)	
GN	AR OR NR3C4 Canis familiaris (Dog)	
OS	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. [1]	
OC	NCBI_TaxID:9615;	
OX		
RN		
RP	SEQUENCE FROM N.A.	
RA	RJ B., Smock S.L., Castellberry T.A., Owen T.A.; RT Molecular cloning and functional characterization of the canine androgen receptor. RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases. CC -!- FUNCTION: steroid hormone and their receptors are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. CC -!- SUBCELLULAR LOCATION: NUCLEAR. CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN. CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY. CC -!- SUBFAMILY: NR3 .	
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CC	DR EMBL; AFA17950; AAF18084; 1. DR InterPro; IPR001103; Androgen_recep. DR InterPro; IPR00536; Hormone_rec_lig. DR InterPro; IPR001628; zf-C4. DR Pfam; PF02166; Androgen_recep; 1. DR Pfam; PF00104; hormone_rec; 1. DR Pfam; PF00105; zf-C4; 1.	
DR	582 SCKVFEKRAAFSGKOKYLCASNRNCTIDKFRKNCPSCLRKCYEAGMTLQARKLKKLGNL 641 566 SCKVFEKRAAGKQKYLCAASNRDCTIDKFRKNCPSCLRKCYEAGMTLQARKLKKLGNL 625 642 KLOQEGEASSTSPTEETTQLTVSHIEGECQFPLDYYFPQKTCILCDEASGCHYGAATCG 581 506 CVKSEMGFWMDSYSGPYGDMRLETARDHVLPLDYYFPQKTCILCDEASGCHYGAATCG 580 462 GCGGGGGGGGGGEAVAPYGTTRPQPLAGQESDFTADPVYPGHMSRVYPSPSP 521 461 DG-----GSVAPYGTTRPQPLAGQEGDFPPDWWPGGVSVRFPSPS 505 522 CVKSEMGFWMDSYSGPYGDMRLETARDHVLPLDYYFPQKTCILCDEASGCHYGAATCG 461 401 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAXQSRDYYNPLALAGPQQPPPHARIKENPLDYSW 401 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 401 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 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ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 341 ELPSTLSSLYKSGLDEAAAYQDRDYYNPLSUGGPPPHPPHTTRIKENPLDYSW 340 Db 402 AAAAQCYRGDLASLHGAGAAGPSSGSPSATSSSHTLTAEGOLYGPQPHPPHTTRIKENPLDYSW 400 342 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C	686	AALLSSNLENGEROLYHVVKWAKALPGFRNLHDQDMAVIQYSNGLMFTAMGNRSTFNV	745
C	762	NSRMLYTFAPDLVNEYRMRHKSRMYSOCVVRMHLHSQEFQWLIQTPQEFCLMKALLFSIIP	821
C	746	NSRMLYTFAPDLVNEYRMRHKSRMYSOCVVRMHLHSQEFQWLIQTPQEFCLMKALLFSIIP	805
C	822	VDGLKNAQKFFDELRYMAYKELDRITACKRKNPNTSCSRRFVYLTQKTLKLDSYOPTARLHQFT	881
C	806	VDGLKNAQKFFDELRYMAYKELDRITACKRKNPNTSCSRRFVYLTQKTLKLDSYOPTARLHQFT	865
C	882	FDLILKSHMVSDFPEMMAEISVQPKTLGSKVKPIYFHQ	923
C	866	FDLILKSHMVSDFPEMMAEISVQPKTLGSKVKPIYFHTQ	907

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T -1: FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN
T THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR
L DIVERSIFICATION AND DIFFERENTIATION IN TARGET TISSUES.
C

PROTEIN AND DNA ENZYME IN SWISS-PROT

- !- SUBCELLULAR LOCATION: NUCLEAR.
- !- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE SPERM VESTICLE, VENTRAL PROSTATE AND COAGULATING GLAND WITH LOWER LEVELS IN THE KIDNEY, AND LEVATOR ANI MUSCLE.
- !- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
- !- DISEASE: DEFECTS IN AR ARE A CAUSE OF ANDROGEN INSENSITIVITY. RATE WITH THE SYNDROME ARE CALLED TESTICULAR FEMINIZED (TFM).
- !- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY, NR3 SUBFAMILY.

Db	397	AAAAQCRTGDLASLHGGSVAGGSTGSPATASSSNHTLTAEGQLYGP-----	445
QY	463	GCGGGGGGGGCGAAGAVAPYTRPQGLAQESDFTADPVYPGGMVSRVPSPTC	522
Db	446	----GGGGSSSSPSDAGPVAPYTRPQGLAQESDFTADPVYPGGMVSRVPSPTC	501
QY	523	VKSEMPWMDSYSPGQCDMRLTARDHVLPIYYFPQKTCILICDEASCHYGA	582
Db	502	VSEMPWMDSYSPGQCDMRLTARDHVLPIYYFPQKTCILICDEASCHYGA	561
QY	583	CKVFFKRAEGKOKYLCASRNCTIDKFRKNCPSCLRKCYEAGMTLGARKKKLGNLK	642
Db	562	CKVFFKRAEGKOKYLCASRNCTIDKFRKNCPSCLRKCYEAGMTLGARKKKLGNLK	621
QY	643	IQEGEASSTSPTETTOKLTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQD	702
Db	622	IQEGENSSAGGTEPSQKMTVSHIEGYEQPIFLNVLEAIEPGVVCAGHDNNQD	681
QY	703	ALLSLNLGEQVHVKWAKALPGERFLNHLDDQAVIYQSWMGLMVFAMGWSFT	762
Db	682	ALLSLNLGEQVHVKWAKALPGERFLNHLDDQAVIYQSWMGLMVFAMGWSFT	741
QY	763	SRMLYFAPDLYFNEYRMHKSRMYSOCYMRHLSOEGFWLQITPQEFLCMKALLLFS	822
Db	742	SRMLYFAPDLYFNEYRMHKSRMYSOCYMRHLSOEGFWLQITPQEFLCMKALLLFS	801
QY	823	DGLKNOKEFDERMNYKELDRILACKRNNTSCSFRYQVLTKLDSVQPTARELHQ	882
Db	802	DGLKNOKEFDERMNYKELDRILACKRNNTSCSFRYQVLTKLDSVQPTARELHQ	861
QY	883	DLLKSHMVSDFPENMAETISVQPKVLSKVKPFLYFHTQ	923
Db	862	DLLKSHMVSDFPENMAETISVQPKVLSKVKPFLYFHTQ	902

RESULT 8

ANDR_MOUSE
ID ANDR_MOUSE
AC P1091;

DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE ANDROGEN RECEPTOR-(DIHYDROTESTOSTERONE RECEPTOR).

GN AR OR NR3C4 .

OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TAXID=10090.

RN SEQUENCE FROM N.A.

RP STRAIN-BALB/C;

RX MEDLINE-90366642; PubMed=2403358;

RA He W.W., Fischer L.M., Sun S., Bilhartz D.L., Zhu X., Young C.Y.F.,

RA Kelley D.B., Tindall D.J.

RT "Molecular cloning of androgen receptors from divergent species with

RT a polymerase chain reaction technique: complete cDNA sequence of the

RT mouse androgen receptor and isolation of androgen receptor cDNA

RT probes from dog, guinea pig and clawed frog.";

RL Biochem. Biophys. Res. Commun. 171:697-704 (1990).

RN SEQUENCE FROM N.A.

RA Gaspar M.L., Meo T., Tosi M.

RT "Structure and size distribution of the androgen receptor mRNA in

RT wild-type and Trif/Y mutant mice;"

RL Mol. Endocrinol. 4:1600-1610 (1990).

RN SEQUENCE FROM N.A.

RA MEDLINE-91354214; PubMed=883316;

RA Faber P.W., King A., van Rooij H.C.J., Brinkmann A.O., de Boer N.J.,

RA Trapman J.;

RT "The mouse androgen receptor. Functional analysis of the protein and

RT	characterization of the gene.";	X
RL	Biochem. J. 278:269-271 (1991).	X
RN	[4]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=22017874; PubMed=1681426;	
RA	Charest F.S.; Zhou Z.; Lubahn D.B.; Olsen K.L.; Wilson E.M.,	
RA	French F.S.;	
RT	"A frameshift mutation destabilizes androgen receptor messenger RNA	
RT	"in the Tm mouse.";	
RL	Mol. Endocrinol. 5:573-581 (1991).	X
CC	-!- FUNCTION: THE STEROID HORMONE(S) AND THEIR RECEPTORS ARE INVOLVED IN	
CC	THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR	
CC	PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.	
CC	-!- SUBCELLULAR LOCATION: NUCLEAR	
CC	-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N TERMINAL DOMAIN,	
CC	A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.	
CC	-!- MISCELLANEOUS: IN THE ABSENCE OF LIGAND, STEROID HORMONE RECEPTORS	
CC	ARE THOUGHT TO BE WEAKLY ASSOCIATED WITH NUCLEAR COMPONENTS;	
CC	HORMONE BINDING GREATLY INCREASES RECEPTOR AFFINITY. THE	
CC	HORMONE-RECEPTOR COMPLEX APPEARS TO RECOGNIZE DISCRETE DNA	
CC	SEQUENCES UPSTREAM OF TRANSCRIPTIONAL START SITES.	
CC	-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.	
CC	NR3 SUBFAMILY.	
CC	-----	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL: S56585; AAB19916.1; -	
DR	EMBL: X53779; CAA37795.1; -	
DR	EMBL: X53780; AAA37234.1; -	
DR	EMBL: X53932; CAA44160.1; -	
DR	PIR: A35695; A35895; -	
DR	PIR: A37255; A37255; -	
DR	PIR: A37708; A37708; -	
DR	PIR: S17198; S17198; -	
DR	PIR: S34398; S34398; -	
DR	HSSP: P0536; 1RGD.	
DR	TRANSFAC: T00041; -	
DR	MGD: MG-188064; Ar.	
DR	InterPro: IPR011103; Androgen_recept.	
DR	InterPro: IPR00536; Hormone_rec_lig.	
DR	InterPro: IPR001628; zf-C4.	
DR	Pfam: PF00104; hormone_rec; 1.	
DR	PF00105; zf-C4; 1.	
DR	PRINTS: PRO0047; STEROID-LINGER.	
DR	PRINTS: PRO00521; ANDROGEN.	
DR	SMART: SM00430; HOLL; 1.	
DR	SMART: SM00398; Znf_C4; 1.	
DR	PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.	
KW	Receptor; Transcription regulation; DNA-binding; Nuclear protein;	
KW	Zinc-finger; Probes; Steroid-binding.	
FT	DOMAIN 1 537 MODULATING (BY SIMILARITY).	
FT	DNA_BIND 539 604 NUCLEAR RECEPTOR-TYPE.	
FT	ZN_FING 539 559 C4-TYPE.	
FT	ZN_FING 575 599 C4-TYPE.	
FT	DOMAIN 670 899 LIGAND-BINDING.	
FT	DOMAIN 63 67 POLY-ARG.	
FT	DOMAIN 174 193 POLY-GLN.	
FT	DOMAIN 367 373 POLY-PRO.	
FT	DOMAIN 391 397 POLY-ALA.	
FT	DOMAIN 441 447 POLY-GLY.	
SEQ	SEQUENCE 899 AA; FD9EE07C0757A568 CRC64;	

Query Match 85.0%; Score 4176; DB 1; Length 899;
 Best Local Similarity 84.18%; Pred. No. 1.3e-190;
 Matches 790; Conservative 40%; Mismatches 53; Indels 56; Caps 5;

DE	ANDROGEN RECEPTOR (DIHYDROTESTOSTERONE RECEPTOR) (FRAGMENT).
GN	OR NR3C4.
OS	Oryctolagus cuniculus (Rabbit)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
OX	NCBI_TAXID9986;
RN	
[1]	SEQUENCE FROM N.A.
RP	STRAIN=NEW ZEALAND WHITE; TISSUE=Prostate;
RC	ORC
RX	Medline= 96044663; PubMed=7559153;
RA	Krönigard A.; Wilson J.D.; McPhaul M.J.;
RT	"Cloning and partial sequencing of the rabbit androgen receptor expression in fetal urogenetic tissues."
RT	J. Androl. 16: 209-214 (1995).
RL	
CC	J. FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EMBRYOTIC GENE EXPRESSION AND AFFECT PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC	-1- SUBCELLULAR LOCATION: NUCLEAR.
CC	-1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC	-1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY NR3 SUBFAMILY.
CC	
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CC	
CC	EMBL: U16366; AAC41469.1; -.
DR	HSSP: P06536; IRGD.
DR	InterPro: IPR01103; Androgen_recep.
DR	InterPro: IPR00536; Hormone_rec_119.
DR	InterPro: IPR001628; zf-C4.
DR	PF02166; Androgen_Recep; 1.
PFAM	PF010104; hormone_rec; 1.
DR	PFAM: PF00105; zf-C4; 1.
DR	SMART: SMD00430; HOLL; 1.
DR	SMART: SMD00399; zf-N4-C4; 1.
DR	PROSITE: PS00031; NUCLEAR RECEPTOR: 1. NUCLEAR RECEPTOR; Transcription regulation; DNA-binding; Nuclear receptor; Zinc-finger; Steroid-binding.
KW	
KW	NON-TER
FT	1 <1 347 MODULATING
FT	DOMAIN 349 414 NUCLEAR RECEPTOR-TYPE.
FT	DNA_BIND 349 414 CA4-TYPE.
FT	ZN_FING 349 369 CA4-TYPE.
FT	ZN_FING 385 409 LIGAND BINDING.
FT	DOMAIN 480 709 POLY-GLN.
FT	DOMAIN 3 6 POLY-PRO.
FT	DOMAIN 182 187 POLY-ALA.
FT	DOMAIN 201 207 POLY-GLY.
FT	DOMAIN 254 262 POLY-GLY.
SEQUENCE	709 AA; 77391 MW; 40E7666137E97B6B CRC64;
SQ	
Query Match	71.4%
Best Local Similarity	90.9%
Matches	16; Mismatches: 1; Indels: 1
Qy	198 QQQQAEVSESSGGRAREASSGSSRDKYNTGGTTISDNKELCKAVSVSMGLG
Db	3 QQQQDAATEGSSSGRARRPSSGASTSSKDSYLSIGTSVISDAKELCKAVSVSMGLG
Qy	258 HLSPGEOLRQDCMAYAPLGYPVAPRTPCAPLAECKGSLDDSAKGKSTDEAAYS
Db	63 HLSSGEOLRGDMAYAPLGYPVAPRTPCAPLAECKGSLDDGPKGTEAETY
Qy	318 YTKGLEGESLGCGSAAAGSSGTLEPLSTLSYKSGALDEAAAYOSRDYNNFPLA
Db	123 YNKGLEAEASLGCGSAAAGSSGTLEPLSTLSYKSGALDEAAAYOSRDYNNFPLA

Db	128	-----QPSPACEVTSNQLFGPELP-----EDPPAAATQRVILSPLMRSGCKVGD 174	RN	SEQUENCE FROM N.A.
Qy	177	SSCSADLKDILSE-ASTMOLL-----QQQQQEAVESEFGSSGRAREASGA 219	RP	SPRAY DAWLEY; TISSUE=Placenta;
Qy	175	SSGTTAAAHKVPLRGLSPARQLLIPASESPHWSGAPVPSQAAVEVEEDEGSESESAG 234	RC	STRAIN=SPRAGUE DAWLEY; PubMed=829566;
Db	220	P-TSSKDNVYLGGTSTISNA-----KELCKAVSVSMGLGVFALEHLSPGE 263	RX	MEIDLINE=94130817; Pubmed=829566;
Qy	235	PLKGKPRALGAAAGGGAAAVPGAAAGGVALPKDSDRSFAPRL-VEQDAPNAPGR 293	RA	Park-Sarge O.K.; Mayo K.E.;
Db	264	QLRG----DCMAYAPLGLGVPPAVPAPCPLAERGSLLDSACKSTEDTAEVSPFRGGYT 319	RA	*Regulation of the progestrone receptor gene by gonadotropins and cyclic adenosine 3',5'-monophosphate in rat granulosa cells.";
Qy	294	SPLATTVMDFIHPII-----PLNHLAIAAFTROLLED-----YDGGAAAS 337	RT	Endocrinology 134: 709-718 (1994).
Db	320	KGLEGEISLGCGS-AAAAGSSCTLELP-----STL-SLY-----KSGALDE 357	RL	-1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
Qy	338	AAFPAPRSPCQASSPVAVGDFPDCAYPPDAEPMDAYPLYSDEQPPALKIKBEEEGA-E 395	CC	-1- SUBCELLULAR LOCATION: NUCLEAR.
Qy	358	AAVAYOSRDIY-----NEPLALAGPPPPPPPHARIKLENPLDYGSAWAAAQQ 407	CC	-1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
Db	396	ASARSARSPRSVLYAGANPAAPDFPFL---GPBPPPLPP-----RATP 431	CC	CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
Qy	408	CRYGDIALSHGAGAAGPGCGSPSANAASSSSWH-----TLETFAE-----EGOLYGPQGGGGGG 459	CC	CC NR3 SUBFAMILY.
Db	432	SRPGE----AAVTAAPASAVSASSASSSSSTLCTLYKAEGAPPQGPFAAPPCKADGAS 486	CC	CC
Qy	460	GGGGGGGGGGGGGGGGGEAGAVAPYGYTRPQHAGQESDFTADFWVYPGGMWSR-VPYP 518	CC	CC
Db	487	GCLLPDPDGLSTSAAAAGA-APALY--PALGLNG-----LPQLGYQAAVILKEGLPQV 537	CC	CC
Qy	519	SPTCYKSEMGPMWDSYSPGVDGMRILETARDHVLPTDYYFP--PDKTCLTCGDAFSGCHY 576	CC	CC
Db	538	YPPYL_NYLREDSSEAQSQP-----QYSPESLPIKICLICGDAFSGCHY 580	CC	CC
Qy	577	ALTGSCSKVFKVRAEGKOKYKLASCNRDCTIDKFRKRKNPSCSLRKCYFAGMFLGARKLK 636	CC	CC
Qy	581	VLTCGSKCKVFKVRAEGHONYLCAGRNDCTIVDKTRRKNCPACLRKCCQAGMVLGGRKF 640	CC	CC
Db	637	KIGNLKIQEEBEASSTSTP-----TEETPQKLTVSHIGYECOPIFLNLEALEPGVVC 690	CC	CC
Qy	641	KENKVKYVVRALDAVLQPLQGVNPESQQLSQRFTPSQGDQDILQPLIPPLNLMLEPDVY 700	CC	CC
Qy	691	AGHDNNQNPDSFAALLSLNEGLEROLVHWDQMAVYKSWMGLMV 750	CC	CC
Db	701	AchDNTKPKDTSSLLSLNQLGRLQVLSVVKWSKLPGRNLHDDQITLQI-SWMSLMV 760	CC	CC
Qy	751	FAMGWRSTFTNNYNSRMLYFAPDLYFNEYRMHKSRTMSYQCVRMHLSQEFQFWLQITPQEFILC 810	CC	CC
Db	761	FGLGWRSKYHQSQMLYFAPDILNQRMKESFSYVSLCLTMWQ1PQEFVKLQVSQEFILC 820	CC	CC
Qy	811	MKALLESITIPDGLKNOKEPDELRMNIEKLDLITACKEKPNP1CSRRYQLTKLDDSY 870	CC	CC
Db	821	MKVLLLNTIPLEGLRSQTSRQEMRSYIRELIRAGLRRGQVSSQRYQLTKLDDNL 880	CC	CC
Qy	871	QPIAREHQHTDILKSHMVSVDPEMMABILISYQVKILLGSKYKPIYFH 921	CC	CC
Db	881	HDLVKQHLHYCLNTFIQSRALSEFEMMSEVIAQLPKTLAGMYKPLLFH 931	CC	CC
Qy	921	VLDLFLAPSPQEQTSPP -ACADATWCLRGELPDPRSVATGQLSPMSRESK 113	CC	CC
Db	966	QAQELPDEKTQNLQSLSDYVEGAFSGVEASRRSRNPAPEKDSRLDS- 113	CC	CC
Qy	1111	VLDEEQPSQPSALECHPERGC-----VPBEGAAYAASRKLPOOLPAPPDE- 157	CC	CC
Db	114	1588 -DDSA-----PSTL-----PGLSSCSADLKD---ILSEA 190	CC	CC
Qy	158	-----PSTL-----PGLSSCSADLKD---ILSEA 190	CC	CC
Db	172	AGDSSGTGAGQKVLPKAVSPRQLLPSGSIAWPGAGYKPSQSPATVEEDEGLLETG 231	CC	CC
Qy	191	STMLQLOQQEAUNSEGSSGRAEASGARTSSKDNLYGTSI -SDNAKELKAVSYSM 249	CC	CC
Db	232	SAGPLIKSKPRALEGMCSGGVTANAPGAAAP-----GGVTLVPKEDSRFSAPVRSLE 284	CC	CC

RESULT 12

PRGR_RAT STANDARD; PRT; 923 AA.

ID PRGR_RAT

AC 063449; 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE PROGERONE RECEPTOR (PR).

GN PRG OR NR3C3.

OS Rattus norvegicus (Rat);

OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;

QY	250	GLGV-----EAELHSLPGEQLRGDCM-----YAPLIGV 277	RT "The chicken progesterone receptor: sequence, expression and functional analysis.";
DB	285	DAPVAPGRSPRSLATTVVDFIHYTILNHALLAARTQLELGDSKDGAAQVFPAPRS 344	RT
QY	278	PPAVPAPLAECKGSLLDSAGKSTED-TAFYSPFKGGYTKGLEGESLGSGSAAA 335	RT
DB	345	PSAPSPPVPCDFPDC---TYPPEPDPKDGPVYGEQQPGKRIKEBE---EGTEAA 396	RN [2]
QY	336	GSSTGLEPLSTLISYKSGALDEAAQYSDRYYNNPLALAGPPP--PPPHARIKLEN 393	RP SEQUENCE FROM N.A.
DB	397	SRS----PRDYL-----AGASAATFPDFPL---PRPRPAPPSRP----- 430	RA MEDLINE-91042592; PubMed=3153474; Connely O.M., Dobson A.D.W., Tsai M.-J., Beattie W.G., Toft D.O., Huckaby C.S., Zarucki T., Schrader W.T., O'Malley B.W.; RA Sequence and expression of a functional chicken progesterone receptor.";
QY	394	PLDYGSAWAAAACRYGDLAS-----LHGAGAACGGGS-----PSAASSSSWH 4 38	RA Mol. Endocrinol. 1: 517-525(1987).
DB	431	----GRA-AVAPSAASVPPSSGSALECYLXKEGAPPTQGFPAPLCKPFAASS---- 481	RN
QY	439	TIFTAAEGQLYGPGC9GGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 498	RP SEQUENCE OF 128-164 FROM N.A.
DB	482	-CLLPRDSLPAAP----- 509	RA MEDLINE-86289413; PubMed=2426779;
QY	499	DFTAPDVWYFGMV-SRVPVPSPTCVKSENGPWNID-----SYSGPYGDMFLPARDH 549	RA Connely O.M., Sullivan W.P., Toft D.O., Birnbaumer M., Cook R.G., Maxwell B.L., Zarucki-Schulz T., Greene G.L., Schrader W.T., O'Malley B.W.; RA Molecular cloning of the chicken progesterone receptor.";
DB	510	----LPLQGYQAAVLDKLQVQY-----PLINYLRPDSEASQSPQYGEFSL----- 552	RN
QY	550	VLPDYYFPQPKTCLICGDEASGCHGALTGCSCKVFKRAAGKQKYLCASRNDCTIDK 609	RP DIFFERENCE BETWEEN FORM 1 AND FORM 2.
DB	553	-----PQKICLICGDEASGCHGALTGCSCKVFKRAMGQHNYLCAGRNDCTIVDK 603	RA MEDLINE-86287271; PubMed=2426697;
QY	610	FRKRNCPSCLRKCYEAGMTLIGARKLKKLGNLQKQE--EGEA--SSTSPSTPBT - -QKL 663	RA Jeltsch J.-M., Quirin-Stricker C., Gronemeyer H., Simpson R.J., Garnier J.M., Jacob F., Chambon P.;
DB	604	IRKRNCPCACRLRKCCAGNLGRKEKEFKENKVKYRMRA LDGVALQPSVAFPNESQTLGORI 663	RA "Cloning of the chicken progesterone receptor receptor.";
QY	664	TVSHLEGYECQPIFLNVLAIEGGVVCAGHDNNQPDSTAIISSLNLNGEROLVHVVKWA 723	RT "The chicken progesterone receptor A and B isoforms are products of an alternative translation initiation event.";
DB	664	TFSPQEIQLVPQIPLNLMSTEDDVYVAGHDNTKPDPSLSSLLTSLNOLGEROLSVVKWS 723	RL J. Biol. Chem. 264:14062-14064(1989).
QY	724	KALPGRFRNHVDDOMAVYIQLVQGMLVYFAMGWRSEFTVNSRMLYFAPDLYFNEYRMHKS R 783	RP SEQUENCE FROM N.A. (ALL FORMS).
DB	724	KSLGFRNLHTDQDITLQYWSNLSMAYFGLGWSYKIVSGQMLYFADLNLNEQRHKELS 783	RA MEDLINE=90154055; PubMed=2303488;
QY	784	MSOCVCRMRLSSEQFGLWQIOTPEBLCMKALILFSTIPDGLKQKOFFDELRMYIKELD 843	RA Jeltsch J.-M., Turcotte B., Garnier J.-M., Lerouge T., Krozowski Z., RA Connely H., Chambon P.;
DB	784	FYSLCLTWWQIPEFVKQVTHBEFLCKMVLLNLNTPLEGRSQSQFEEMRSYIRELI 843	RA "Characterization of multiple mRNAs originating from the chicken progesterone receptor gene. Evidence for a specific transcript encoding form A.";
QY	844	RITACKRKNPNTSOSRREYFQLTKLDSVQPIARELHQFTDLKLISMSVSDPEPMMAII 903	RL J. Biol. Chem. 265:3967-3974(1990).
DB	844	KATCLQRQGVPPSQRQYQLTKLDSVQPIARELHQFTDLKLISMSVSDPEPMMAII 903	CC -1- FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
QY	904	SVQPKTILISGKVPIYFH 921	CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; A (SHOWN HERE), A', B AND B';
DB	904	AAQPKTILAGMYKPLLFH 921	CC -1- PRODUCED BY ALTERNATIVE SPLICING.
OS			CC -1- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
RESULT	13		CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
PRGR_CHICK			CC
ID	PRGR_CHICK	STANDARD;	CC
AC	P07812;	PRT; 786 AA.	CC
DT	01-AUG-1988 (Rel. 08, Created)		CC
DT	20-AUG-1988 (Rel. 08, Last sequence update)		CC
DE	PROGESTERONE RECEPTOR (PR).		CC
GN	PGR OR NR3C3.		CC
OS	Galus gallus (Chicken).		CC
Archosauria; Aves; Neognathae; Galliformes; Phasianinae;			CC
OC			CC
NCBI_TAXID	9031;		CC
RN			CC
RP	SEQUENCE FROM N.A.		CC
MEIDLINE	88166640;	PubMed=3443098;	CC
RA	Gronemeyer H., Turcotte B., Quirin-Stricker C., Bocquel M.T., Mayer M.E., Krozowski Z., Jeltsch J.M., Lerouge T., Garnier J.M., Chambon P.;		CC
RA			DR
RA			EMBL; M14280; AAA49039_1;
RA			DR
RA			EMBL; M32732; AAA49011_1;
RA			DR
RA			EMBL; M32726; AAA49011_1; JOINED.

PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.

Job time: 386 sec

CC -!- SUBCELLULAR LOCATION: NUCLEAR.

CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,

CC -!- A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.

CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

CC -!- NR3 SUBFAMILY.

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CC EMBL; 266555; CAP91447.1; - .
 DR HSSP; P06401; 1A28.
 DR InterPro; IPR00536; Hormone_rec_lig.
 DR InterPro; IPR00128; Progest_receptor.
 DR InterPro; IPR001628; zf-C4.
 DR PFam; PF00104; hormone_rec; 1.
 DR Pfam; PF02161; Prog_receptor; 1.
 DR SMART; SM00430; HOLL; 1.
 DR SM00399; ZNF_C4; 1.
 DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
 DR Receptor; Transcription regulation; DNA-binding; Nuclear protein;
 KW Zinc-finger; Steroid-binding.
 FT NON_TER 1 1 .
 FT DOMAIN <1 15 MODULATING, PRO-RICH.
 FT DNA_BIND 18 83 NUCLEAR RECEPTOR-TYPE.
 FT ZN_FING 18 38 C4-TYPE.
 FT ZN_FING 54 78 C4-TYPE.
 FT DOMAIN 128 >77 STEROID-BINDING.
 FT NON_TER 377 377
 SQ 377 AA; 42904 MW; 3141B65587F7493C CRC64;

Query Match 22.7%; Score 1116; DB 1; Length 377;
 Best Local Similarity 55.2%; Pred. No. 1.9e-16;
 Matches 201; Conservative 73; Mismatches 84; Indels 6; Gaps 1;

Qy 559 POKTCLICGDSASGCHYALTGCKVFKRAEERQKYLCASRNDCTIDKFRRKNCPS 618
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 14 PQKICLICGDEASGCHYGVLTGCKVFKRAEERQHNYLCAGRNDCTIVDKIRRKNCPAC 73
 Qy 619 RLRLCYEAGMTLIGARKLKLCLNKLQEEGAEASTSP-----TEETTOKLTYSHIEYE 672
 ||||| :||| ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 74 RIRKCCQAGMVLGGRFKKFNKVRMRTLDALVALFQPGVIGPNEQSALSORITSPSQDIQ 133

Qy 673 CQPIFLNLEALEPGVYCAHDNNOPDSFAALLSSNLNEGERQVHVVKAWALPGFRNL 732
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 134 LIPPLINLMSTEPDMDVYAGHDNSKPDTSSSLNLQGEROLLSVYKWSKSLPGFRNL 193
 Qy 733 HVDQMAVIOQYSWGLMVFAMGWSRPTVNSRMLYFAPDLYFNEYRMRHKSRMYSQCVRMR 792
 ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 194 HIDDQTLIQLYSWMSLWVFGWRSYKHYSGQMLYFAPDILNEQRMKESSTFSCLTMW 253
 Qy 793 HLSQEFGLWQITPQEFGLCKMALKLFLSITIPVGDKNKEFFDELRYNIKELDRLIACKRN 852
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 254 QIPQEFVKLQYSQEEFLCMKVLLNTIPLEGLRSQNQFEMRSYFIRELIKAGLROG 313

Qy 853 PTSCSRFRYQLTKLDSVQPTARELHQFTEDLLKSHMSVYDFSEMMARLISYQVPKLL 912
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 314 VVPSSORFYQLTKLDDNLHDVQHLCLNTFTQSRALSVEFEMMSEVIAQLPKLLA 373
 Qy 913 GKV 916
 | |
 Db 374 GMV 377

